s. O (Rev. 9-27-95)

INTERFERENCE INITIAL MEMORANDUM

Count # 1

BOARD OF PATENT APPEALS AND INTERFERENCES: An interference is found to exist between the following cases:

This interference involves 2 parties

PARTY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY
Yue et al.	08/857,217	5-15-97		

If application has been patented, have maintenance fees been paid? ___Yes ___No ___Maintenance fees not due yet

**Accorded the benefit of:

COUNTRY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY

The claim(s) of this party which correspond(s) to this count is(are):

PATENTABLE CLAIMS: 2, 4-10, 19 — UNPATENTABLE CLAIMS: None

The claim(s) of this party which does(do) not correspond to this count is(are):

PATENTABLE CLAIMS: 20 — UNPATENTABLE CLAIMS: None

PARTY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY
Leung et al.	08/842,827	4-17-97		

If application has been patented, have maintenance fees been paid? ___Yes ___No ___Maintenance fees not due yet

**Accorded the benefit of:

COUNTRY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY

The claim(s) of this party which correspond(s) to this count is(are):

PATENTABLE CLAIMS: 1, 4, 14 — UNPATENTABLE CLAIMS: 3, [illegible]

The claim(s) of this party which does(do) not correspond to this count is(are):

PATENTABLE CLAIMS: 2, 6-9, 15, 16 — UNPATENTABLE CLAIMS: 5, 10-13

Instructions

1. For every patent involved in the interference, check if the fees have been paid by using the **patent number** with the PALM screen CR06.
   If fees are due and they have not been paid, the interference cannot be declared since it would invovlve an expired patent. (35 USC 135(a); 37 CFR 1.606).
2. For each party, separately identify the patentable and unpatentable claims which correspond to the count. (37 CFR 1.601 (f), 1.601 (n), 1.609(b)(2)).
3. For each party, separately identify the patentable and unpatentable claims which do not correspond to the count (37 CFR 1.609(b)(3)).
4. Forward all files including those the benefit of which is being accorded.
5. Keep a copy of the Interference Initial Memorandum and any attachments for your records.

All information requested below must be attached on (a) separate sheet(s) and type-written.

6. On a separate sheet, set forth a single proposed interference count. If any claim of any party is exactly the same word for word as this count, please indicate the party, application or patent number, and the claim number.
7. For each claim designated as corresponding to the count, provide an explanation of why each claim defines the same patentable invention (37 CFR 1.609(b)(2)).
8. For each claim designated as not corresponding to the count, provide an explanation of why each claim defines a separate patentable invention (37 CFR 1.609(b)(3)).
9. For each additional count, if any, repeat steps 2-6 and, additionally, provide an explanation why each count represents a separate patentable invention from every other count (37 CFR 1.609(b)(1)).

DATE	PRIMARY EXAMINER (Signature)	TELEPHONE NO.	ART UNIT
5/13/02	Rebecca Prouty	703-308-4000	1652
DATE 1/6/04	GROUP DIRECTOR SIGNATURE (if required) Wm Woodward		

**The serial number and filing date of each application the benefit of which is intended to be accorded must be listed. It is not sufficient to merely list the earliest application if there are intervening applications necessary for continuity.

THIS PAGE CAN BE DUPLICATED IF THERE ARE MORE THAN TWO INTERFERING PARTIES.

Count 1:

A isolated and purified polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:1 of 08/857,217 and SEQ ID NO:2 of 08/842,827.

This count is identical to Claim 2 of 08/857,217 and Claim 14 of 08/842,827. Claim 1 of 08/842,827 is also identical in scope to the count merely further reciting an inherent property of the polypeptide and thus including some additional non-limiting language.

Claims corresponding to the count:

Claim 2 corresponds to the count as it is identical to the count.

Claim 4 corresponds to the count as it recites a composition comprising the nucleic acids of the count. As the use of the nucleic acid of the count to produce the encoded human phosphatidic acid phosphatase would require the nucleic acid of the count to be solubilized, it would have been obvious to one of ordinary skill in the art to add water or a suitable buffer to the nucleic acid of the count to make a composition as claimed.

Claim 5 corresponds to the count as it recites a nucleic acid species within the genus of the count.

Claims 6 and 7 correspond to the count as they recite nucleic acids having a complementary sequence to the nucleic acids of the count and compositions thereof. A nucleic acid clearly suggests to the ordinary skilled artisan its complementary sequence because the known double helix structure of DNAs requires any DNA comprising a particular sequence to also comprise its complementary sequence as well. As such a nucleic acid complementary to the nucleic acids of the count would have been prima facie obvious to one of ordinary skill in the art as such sequences are well known to be useful as probes for the complementary sequences (i.e., the nucleic acids of the count).

Claims 8-10 correspond to the count as they recite expression vectors comprising the nucleic acids of the count, host cell transformed with the nucleic acids of the count and methods of expressing the nucleic acids of the count.

Kai et al. teach the isolation of porcine PAP, the isolation of and expression of the mouse PAP gene and that PAPs are important enzymes in glycerolipid biosynthesis as well as signal transduction pathways. Therefore, as the nucleic acid of the count encodes a human PAP, it would have been prima facie obvious to one of ordinary skill in the art to insert the nucleic acids of the count into any known expression vector, to transform this vector into any known host cell, and to culture the host cell and

isolate the protein produced in order to obtain the a human protein that would be reasonably expected to have a role in glycerolipid biosynthesis and/or signal transduction pathways.

Claim 19 corresponds to the count it recites a method of detecting a nucleic acid of the count with the nucleic acids of Claim 6. Kai et al. teach the isolation of porcine PAP, the isolation of and expression of the mouse PAP gene and that PAPs are important enzymes in glycerolipid biosynthesis as well as signal transduction pathways. Study of the signal transduction pathways which utilize the nucleic acids of the count would require a means of detecting when the nucleic acids of the count are expressed and in which cell types they are expressed. Therefore, one of ordinary skill would have been motivated to use the nucleic acids of Claim 6 to probe a biological sample for the nucleic acids of the count as doing so would provide a means of identifying those cells expressing the nucleic acids of the count.

Claims not corresponding to the count:

Claim 20 does not correspond to the count as it recites proteins which are patentably distinct compounds from the nucleic acids of the count.

The nucleic acids of the count and the protein of Claim 20, are patentably distinct compounds because they are chemically

different, the DNA has other utility besides encoding the proteins such as a hybridization probe and the proteins can be made by another method such as isolation from natural sources or chemical synthesis.

Count 1:

A isolated and purified polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:1 of 08/857,217 and SEQ ID NO:2 of 08/842,827.

This count is identical to Claim 2 of 08/857,217 and Claim 14 of 08/842,827. Claim 1 of 08/842,827 is also identical in scope to the count merely further reciting an inherent property of the polypeptide and thus including some additional non-limiting language.

Claims corresponding to the count:

Claim 1 corresponds to the count as it is identical in scope to the count merely further reciting an inherent property of the polypeptide and thus including some additional non-limiting language.

Claim 3 corresponds to the count as it recites a method of expressing nucleic acids encoding human phosphatidic acid phosphatases which include the nucleic acids of the count.

Kai et al. teach the isolation of porcine PAP, the isolation of and expression of the mouse PAP gene and that PAPs are important enzymes in glycerolipid biosynthesis as well as signal

transduction pathways. Therefore, as the nucleic acid of the count encodes a human PAP, it would have been prima facie obvious to one of ordinary skill in the art to insert the nucleic acids of the count into any known expression vector, to transform this vector into any known host cell, and to culture the host cell and isolate the protein produced in order to obtain the a human protein that would be reasonably expected to have a role in glycerolipid biosynthesis and/or signal transduction pathways.

However, this claim is not patentable because the scope of the nucleic acids encoding human phosphatidic acid phosphatases which may be used is not limited to the nucleic acids of the count (i.e., encoding a specific human phosphatidic acid phosphatase) but include the use of prior art human phosphatidic acid phosphatase genes such as that of GENBANK entry U79294 as well or the human gene suggested by GENBANK entries AA040858, W04968 or H68363.

GENBANK entry U79294 teaches a cDNA sequence from a human brain library. This cDNA is identical to bases 225-1362 of SEQ ID NO:6 except for a single base deletion encompassing all of the coding sequence of SEQ ID NO:5. This cDNA also exhibits 62% sequence identity with the mouse cDNA encoding PAP of Kai et al.

Kai et al. teach the isolation of porcine PAP, the isolation of and expression of the mouse PAP gene and that PAPs are

important enzymes glycerolipid biosynthesis as well as signal transduction pathways.

In view of the sequence identity between the cDNA of GENBANK entry U79294 and the mouse PAP cDNA of Kai et al, it would have been obvious to one of ordinary skill in the art that the cDNA disclosed by GENBANK entry U79294 encodes a human PAP-like protein. Therefore, it would have been obvious to one of ordinary skill in the art to insert the cDNA of GENBANK entry U79294 into an expression vector and express the encoded protein in order to produce antibodies to a human protein that would be reasonably expected to have a role in glycerolipid biosynthesis and/or signal transduction pathways.

Each of GENBANK entries W04968, H68363, and AA040858 disclose a fragment of human cDNA which comprises a sequence highly homologous to a portion of the sequence of the mouse PAP gene disclosed by Kai et al. It is well known in the art that each EST corresponds to the production of some protein as ESTs are fragments of cDNAs which are produced by reverse transcription from mRNAs of a particular cell type. Only expressed proteins have corresponding mRNAs in a cell and thus each EST corresponds to an expressed protein. While a EST encodes only a portion of the cDNA encoding a particular protein, each EST clearly provides a suggestion that the cell from which

the EST was reverse transcribed expressed a corresponding protein. The high homology of the cited ESTs to the mouse PAP gene disclosed by Kai et al. clearly suggests that the protein to which each of these ESTs correspond is the human homolog of the protein of Kai et al. As such it would have been obvious to one of ordinary skill in the art that there is a human homolog of the PAP of Kai et al. which is highly homologous to the mouse and porcine proteins.

Therefore, as Kai et al. teach that type 2 PAPs such as that encoded by the disclosed gene play a role in the regulation of signal transduction by phospholipase D, it would have been obvious to one of ordinary skill in the art to isolate the gene encoding the human homolog of the porcine and mouse PAPs disclosed by Kai et al., to recombinantly express this gene to produce the human PAP and to use this enzyme for the dephosphorylation of phosphatidic acid and the regulation of signal transduction.

Claim 4 corresponds to the count as it recites a method of expressing the nucleic acids of the count.

Kai et al. teach the isolation of porcine PAP, the isolation of and expression of the mouse PAP gene and that PAPs are important enzymes in glycerolipid biosynthesis as well as signal

transduction pathways. Therefore, as the nucleic acid of the count encodes a human PAP, it would have been prima facie obvious to one of ordinary skill in the art to insert the nucleic acids of the count into any known expression vector, to transform this vector into any known host cell, and to culture the host cell and isolate the protein produced in order to obtain the a human protein that would be reasonably expected to have a role in glycerolipid biosynthesis and/or signal transduction pathways.

Claim 14 corresponds to the count as it is identical to the count.

Claims not corresponding to the count:

Claims 2, and 5-13 do not correspond to the count as they recite proteins or methods of use thereof which are patentably distinct compounds from the nucleic acids of the count.

The nucleic acids of the count and the proteins of Claims 2, and 5-13 are patentably distinct compounds because they are chemically different, the DNA has other utility besides encoding the proteins such as a hybridization probe and the proteins can be made by another method such as isolation from natural sources or chemical synthesis. Furthermore, Claims 7-9 are further distinct as they recite methods of use of human phosphatidic acid phosphatases different in structure from the human PAP encoded by the nucleic acid of the count. The disclosure of one human

phosphatidic acid phosphatase (such as that encoded by the nucleic acid of the count) in no way suggests to the ordinary skilled artisan that another structurally different human phosphatidic acid phosphatase of a defined specific structure exists.

Claims 15 and 16 do not correspond to the count as they recite nucleic acids encoding human phosphatidic acid phosphatases or methods of use thereof which are structurally distinct from the nucleic acids of the count as they encode human phosphatidic acid phosphatases with chemically different amino acid sequences. The disclosure of one human phosphatidic acid phosphatase gene (such as that of the count) in no way suggests to the ordinary skilled artisan that another structurally different human gene of a defined specific structure exists.